

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Horwath, K. L., et al.
- (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Dr. Kathleen L. Horwath
 - (B) STREET: Department of Biological Sciences, Binghamton University
 - (C) CITY: Binghamton
 - (D) STATE: New York
 - (E) ZIP: 13902-6000
- (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 - (B) COMPUTER: IBM AT/ATX compatible
 - (C) OPERATING SYSTEM: Windows 95/98
 - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: 60210446
 - (B) FILING DATE: June 8, 2000
- (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: Mark Levy, Attorney-at-Law
 - (B) REGISTRATION NUMBER: 29,188
 - (C) REFERENCE/DOCKET NUMBER: RB125
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 607-722-6600
 - (B) TELEFAX: 607-724-2207

09876348-060701

(2) INFORMATION FOR SEQ. ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(ix) FEATURES:

- (D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.8b

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val
 1 5 10 15

09876543210-060701

(2) INFORMATION FOR SEQ. ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Non-his-tagged, signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

GTGGATCCAA AGAATTCGGC ACGAGACTAC TAAG ATG AAG TTG CTC      36
                               Met Lys Leu Leu
                               -15

TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG      81
Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu
-10 -5 1

ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT     126
Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
5 10 15

CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC     171
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
20 25 30

AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT     216
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
35 40 45

TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG     261
Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val
50 55 60

GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC     306
Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn
65 70 75

GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA     351
Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg
80 85 90

GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG     396
Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met
95 100 105

AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCACGA          439
Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *
110 115

CTAGTAGATG GTTCAAAATGG TGTGCTTTAC ATATAAAAAT AAAGTGTTC          489

TGATGTAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGAG TATTCTAGAG          539

CGGCCGCGGG CCCATCGTTT TCCACCC                                566

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(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

Met Lys Leu Leu Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val
   -15                      -10                      -5

Gln Ala Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys
    1                      5                      10

Lys Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala
  15                      20                      25                      30

Arg Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
   35                      40                      45

Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val
   50                      55                      60

Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu
   65                      70                      75

Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val
   80                      85                      90

Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro
   95                      100                      105                      110

Lys Phe Ser Pro Val Asp *
                      115

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09876343.060701

(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
1      5      10      15
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn
20     25     30
Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val
35     40     45
Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp
50     55     60
Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr
65     70     75     80
Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu
85     90     95
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe
100    105    110
Ser Pro Val Asp *
115

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0976348-060701

(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGC	ACG	GAG	CA	AAA	ATG	AAA	CTC	CTC	TTG	TGC	TTT	GCG	TTC	GCC	GCC	46
					Met	Lys	Leu	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala	
							-15								-10	
ATC	GTC	ATC	GGA	GCT	CAG	GCT	CTC	ACC	GAC	GAA	CAG	ATA	CAG	AAA		91
Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys		
			-5				1				5					
AGG	AAC	AAG	ATC	AGC	AAA	GAA	TGC	CAG	CAG	GTG	TCC	GGA	GTG	TCC		136
Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser		
			10				15							20		
CAA	GAG	ACG	ATC	GAC	AAA	GTC	CGC	ACA	GGT	GTC	TTG	GTC	GAT	GAT		181
Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	Asp		
			25				30							35		
CCC	AAA	ATG	AAG	AAG	CAC	GTC	CTC	TGC	TTC	TCG	AAG	AAA	ACT	GGA		226
Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	Gly		
			40				45							50		
GTG	GCA	ACC	GAA	GCC	GGA	GAC	ACC	AAT	GTG	GAG	GTA	CTC	AAA	GCC		271
Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala		
			55				60							65		
AAG	CTG	AAG	CAT	GTG	GCC	AGC	GAC	GAA	GAG	GTG	GAC	AAG	ATC	GTG		316
Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	Ile	Val		
			70				75							80		
CAG	AAG	TGC	GTG	GTC	AAG	AAG	GCC	ACA	CCA	GAG	GAA	ACG	GCT	TAT		361
Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	Tyr		
			85				90							95		
GAC	ACC	TTC	AAG	TGT	ATT	TAC	GAC	AGT	AAA	CCT	GAT	TTC	TCT	CCT		406
Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	Pro		
			100				105							110		
ATT	GAT	TAA	TTG	TTT	TGTA	TTT	GACT	GAA	TTT	GACA	AT	AA	AGG	TAATA		455
Ile	Asp	*														
			115													
TCG	TTAT	GTA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	481

- (2) INFORMATION FOR SEQ. ID NO: 6
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Non-His-tagged, Signal plus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC	46
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala	
-15 -10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5 1 5	
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	
10 15 20	
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25 30 35	
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly	
40 45 50	
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55 60 65	
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG	316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	
70 75 80	
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	
85 90 95	
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	
100 105 110	
ATT GAT TAA TTGTTTGTG TTTGACTGAA TTTTGACAAT AAAGGTACTA	455
Ile Asp *	
115	
TCGTTATGAA AAAAAAAAAA AAAAAAA	482

(2) INFORMATION FOR SEQ. ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
    -15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
    1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
  15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
    35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
    50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
    65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
    80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
    95                      100                      105                      110

Phe Ser Pro Ile Asp *
                      115

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09876348-060701

(2) INFORMATION FOR SEQ. ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1      5      10      15
Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20     25     30
Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35     40     45
Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50     55     60
Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
65     70     75     80
Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85     90     95
Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100    105    110
Pro Ile Asp *
115

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F02090-245-060701

(2) INFORMATION FOR SEQ. ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCACGAGCA	AAA	ATG	AAA	CTC	CTC	TTG	TGC	TTT	GCT	TTC	GCC	GCC	46
	Met	Lys	Leu	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala		
				-15								-10	
ATC	GTC	ATC	GGA	GCT	CAG	GCT	CTC	ACC	GAC	GAA	CAG	ATA	41
Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	
			-5				1				5		
AGG	AAC	AAG	ATC	AGC	AAA	GAA	TGC	CAG	CAG	GTG	TCC	GGA	136
Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	
			10				15				20		
CAA	GAG	ACG	ATC	GAC	AAA	GTC	CGC	ACA	GGT	GTC	TTG	GTC	181
Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	
			25				30				35		
CCC	AAA	ATG	AAG	AAG	CAC	GTC	CTC	TGC	TTC	TCG	AAG	AAA	226
Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	
			40				45				50		
GTG	GCA	ACC	GAA	GCC	GGA	GAC	ACC	AAT	GTG	GAG	GTA	CTC	271
Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	
			55				60				65		
AAG	CTG	AAG	CAT	GTG	GCC	AGC	GAC	GAA	GAG	GTG	GAC	AAG	316
Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	
			70				75				80		
CAG	AAG	TGC	GTG	GTC	AAG	AAG	GCC	ACA	CCA	GAG	GAA	ACG	361
Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	
			85				90				95		
GAC	ACC	TTC	AAG	GTT	ATT	TAC	GAC	AGT	AAA	CCT	GAT	TTC	406
Asp	Thr	Phe	Lys	Val	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	
			100				105				110		
ATT	GAT	TAA	TTGTTTTGTA	TTTGACTGAA	TTTTGACAAT	AAAGGTACTA							455
Ile	Asp	*											
			115										
TCGTTATGTA	AAAAAAAAAA	AAAAAA											481

- (2) INFORMATION FOR SEQ. ID NO: 10
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vi) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein for Clone 3.4
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
  -15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
   1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp
 95                      100                      105                      110

Phe Ser Pro Ile Asp *
                      115

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F02090-040340-060704

- (2) INFORMATION FOR SEQ. ID NO: 11
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Mature Protein for Clone 3.4
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1          5          10          15
Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20          25          30
Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35          40          45
Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50          55          60
Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
65          70          75          80
Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85          90          95
Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100         105         110
Pro Ile Asp *
115

```

0907E340-060701

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC 46
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
-15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA 91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
-5 1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC 136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser
10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT 181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA 226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly
40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG 316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
85 90 95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
100 105 110

ATT GAT TAA TTGTTTGTG TTTGACTGAA TTTTGACAAT AAAGGTACTA 455
Ile Asp *
115

TCGTTATGAA AAAAAAAAAA AAAAAAA 482

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3.9

(D) OTHER INFORMATION: Precursor Protein for Clone 3.9

Phe Ser Pro Ile Asp *
115

(2) INFORMATION FOR SEQ. ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Mature protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1      5      10      15
Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20      25      30
Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35      40      45
Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50      55      60
Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu Val Asp
65      70      75      80
Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85      90      95
Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100     105     110
Pro Ile Asp *
115

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09076348-060701

(2) INFORMATION FOR SEQ. ID NO: 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Non-his-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      90
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
    10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
    25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
    40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
    55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
    70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
    85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
   100                      105                      110

ATT GAT TAA TTGTTTGTGTA TTTGGCTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
   115

TCGTTATGTA AAAAAAAAAA AAAAAA      481

```


- (2) INFORMATION FOR SEQ. ID NO: 16
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

09876348-060701
T07090"84E92860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

T02990.84297860

(2) INFORMATION FOR SEQ. ID NO: 17

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *

105 110 115

(2) INFORMATION FOR SEQ. ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	



(2) INFORMATION FOR SEQ. ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
95 100 105 110

Phe Ser Pro Ile Asp *
115

- (2) INFORMATION FOR SEQ. ID NO: 20
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal Plus

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T02030-84E92860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
TTTGA CTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA	645
AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT	682

T02090"84E9860

(2) INFORMATION FOR SEQ. ID NO: 21
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 Amino Acids
 (B) TYPE: Amino Acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: Protein
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Tenebrio molitor*
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 2.3
 (ix) FEATURES
 (D) OTHER INFORMATION: Precursor Protein with His-tag
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	-55	-50	-45	
Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	-40	-35	-30	
Gly	Ser	Glu	Phe	Ala	Arg	Ala	Lys	Met	Lys	Leu	Leu	Leu	Cys	Phe	Ala	-25	-20	-15	
Phe	Ala	Ala	Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	-10	-5	1	5
Gln	Lys	Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	10	15	20	
Ser	Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	25	30	35	
Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	Gly	Val	40	45	50	
Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala	Lys	Leu	55	60	65	70
Lys	His	Val	Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	Ile	Val	Gln	Lys	Cys	75	80	85	
Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	Tyr	Asp	Thr	Phe	Lys	90	95	100	
Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	Pro	Ile	Asp	*			105	110	115	

09876348-060701

- (2) INFORMATION FOR SEQ. ID NO: 22
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
- (B) CLONE: 2.3
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
   -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
    1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
   15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
   35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
   50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
   65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
   80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
   95                      100                      105                      110

Phe Ser Pro Ile Asp *
   115

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09676348-060701

- (2) INFORMATION FOR SEQ. ID NO: 24
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

09876348-060701

RB125 RT

(2) INFORMATION FOR SEQ. ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
  -55                      -50                      -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
  -40                      -35                      -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile
  -25                      -20                      -15                      -10

Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
          -5                      1                      5

Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val
          10                      15                      20

Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp
          25                      30                      35

Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu
          40                      45                      50

Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val
          55                      60                      65                      70

Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys
          75                      80                      85

Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe
          90                      95                      100

Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *
          105                      110                      115

```

09876348-060701

- (2) INFORMATION FOR SEQ. ID NO: 26
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA	186
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	
-5 1 5	
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG	231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	
10 15 20	
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT	276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	
25 30 35	
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT	321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	
40 45 50	
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG	366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	
55 60 65	
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC	411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	
70 75 80	
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG	456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	
85 90 95	
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA	501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	
100 105 110	
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Val Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
   -30                               -25                               -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -15                               -10                               -5

Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys
   1                               5                               10                               15

Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
   20                               25                               30

Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys
   35                               40                               45

Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val
   50                               55                               60

Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu
   65                               70                               75

Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu
   80                               85                               90                               95

Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys
   100                              105                              110

Phe Ser Pro Val Asp *
   115

```

1070990-848348-060701

(2) INFORMATION FOR SEQ. ID NO: 28

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 681 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Tenebrio molitor
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 3.4
(ix) FEATURES
 (D) OTHER INFORMATION: His-tagged, Signal plus
```



RB125 RT

- (2) INFORMATION FOR SEQ. ID NO: 29
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 173 Amino Acids
    - (B) TYPE: Amino Acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Protein
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 3.4
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Precursor protein with His-tag
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100

Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
 105 110 115

```

09876348-060704

## (2) INFORMATION FOR SEQ. ID NO: 30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

|                                                             |     |
|-------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG      | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  | 96  |
| Met Gly Ser Ser His His His His His His Ser                 |     |
| -30 -25                                                     |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly |     |
| -20 -15 -10                                                 |     |
| GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln |     |
| -5 1 5                                                      |     |
| AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG | 231 |
| Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val |     |
| 10 15 20                                                    |     |
| TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC | 276 |
| Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp |     |
| 25 30 35                                                    |     |
| GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT | 321 |
| Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr |     |
| 40 45 50                                                    |     |
| GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA | 366 |
| Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys |     |
| 55 60 65                                                    |     |
| GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC | 411 |
| Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile |     |
| 70 75 80                                                    |     |
| GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT | 456 |
| Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala |     |
| 85 90 95                                                    |     |
| TAT GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT | 501 |
| Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser |     |
| 100 105 110                                                 |     |
| CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT            | 543 |
| Pro Ile Asp *                                               |     |
| 115                                                         |     |

## (2) INFORMATION FOR SEQ. ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
                  -30                                  -25                                          -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

- (2) INFORMATION FOR SEQ. ID NO: 32
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 682 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 3.9
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal plus

09976348.060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

|                                                                                                                            |     |
|----------------------------------------------------------------------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG                                                                     | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC<br>Met Gly Ser Ser His His His His His His Ser                  | 96  |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT<br>Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly | 141 |
| GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG<br>Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met | 186 |
| AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT<br>Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala | 231 |
| CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC<br>Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser | 276 |
| AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC<br>Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp | 321 |
| AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG<br>Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys | 366 |
| CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC<br>His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala | 411 |
| GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG<br>Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val | 456 |
| GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC<br>Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val | 501 |
| AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT<br>Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys | 546 |
| ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA<br>Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *       | 595 |
| TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA                                                                     | 645 |
| AAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT                                                                                    | 682 |

09076343-060704  
 09076343-060704

## (2) INFORMATION FOR SEQ. ID NO: 33

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
                   -55                  -50                  -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
                   -40                  -35                  -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala  
                   -25                  -20                  -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
                   -10                  -5                  1                  5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val  
                   10                  15                  20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
                   25                  30                  35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val  
                   40                  45                  50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
                   55                  60                  65                  70

Lys HisVal Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
                   75                  80                  85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
                   90                  95                  100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
                   105                  110                  115

09876348 "060701

- (2) INFORMATION FOR SEQ. ID NO: 34
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 543 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 3.9
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal minus
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

|                                                             |     |
|-------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG      | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  | 96  |
| Met Gly Ser Ser His His His His His His Ser                 |     |
| -30 -25                                                     |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly |     |
| -20 -15 -10                                                 |     |
| GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAT GAA CAG ATA CAG | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln |     |
| -5 1 5                                                      |     |
| AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG | 231 |
| Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val |     |
| 10 15 20                                                    |     |
| TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC | 276 |
| Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp |     |
| 25 30 35                                                    |     |
| GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT | 321 |
| Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr |     |
| 40 45 50                                                    |     |
| GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA | 366 |
| Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys |     |
| 55 60 65                                                    |     |
| GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC | 411 |
| Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile |     |
| 70 75 80                                                    |     |
| GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT | 456 |
| Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala |     |
| 85 90 95                                                    |     |
| TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT | 501 |
| Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser |     |
| 100 105 110                                                 |     |
| CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT            | 543 |
| Pro Ile Asp *                                               |     |
| 115                                                         |     |



## (2) INFORMATION FOR SEQ. ID NO: 35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

```

09076348-060704  
T02090-04092060

- (2) INFORMATION FOR SEQ. ID NO: 36
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 681 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 7.5
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal plus

09876348-060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

|                                                                                                                                           |     |
|-------------------------------------------------------------------------------------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG                                                                                    | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC<br>Met Gly Ser Ser His His His His His His Ser<br>-55 -50                          | 96  |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT<br>Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly<br>-45 -40 -35 | 141 |
| GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG<br>Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met<br>-30 -25 -20 | 186 |
| AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT<br>Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala<br>-15 -10 -5  | 231 |
| CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC<br>Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser<br>1 5 10      | 276 |
| AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC<br>Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp<br>15 20 25    | 321 |
| AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG<br>Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys<br>30 35 40    | 366 |
| CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC<br>His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala<br>45 50 55    | 411 |
| GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG<br>Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val<br>60 65 70    | 456 |
| GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC<br>Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val<br>75 80 85    | 501 |
| AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT<br>Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys<br>90 95 100   | 546 |
| ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA<br>Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *<br>105 110 115        | 595 |
| TTTGGCTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAAA                                                                                    | 645 |
| AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT                                                                                                   | 681 |

D9876343.DEC701

## (2) INFORMATION FOR SEQ. ID NO: 37

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

## (ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
 105 110 115

```

09076348-060701

## (2) INFORMATION FOR SEQ. ID NO: 38

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 7.5

## (ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal minus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96
 Met Gly Ser Ser His His His His His His Ser
 -30 -25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
 -20 -15 -10

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG 186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln
 -5 1 5

AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG 231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC 276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp
 25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT 321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr
 40 45 50

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys
 55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC 411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile
 70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
 85 90 95

TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
 100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT 543
Pro Ile Asp *
 115

```

## (2) INFORMATION FOR SEQ. ID NO: 39

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Mature protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

```

09876348-060701

## (2) INFORMATION FOR SEQ. ID NO: 40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5

## (ix) FEATURES

- (D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-H1 site

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG 24

09876343-060701

- (2) INFORMATION FOR SEQ. ID NO: 41
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Tm 12.84 lower primer with XhoI site
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAA CTAATTGAGC TCGCC 25

09876349-060701  
T02090-8492860



## (2) INFORMATION FOR SEQ. ID NO: 42

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (v)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

## (ix) FEATURES

- (D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-H1 site

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGCGGATCCC TGACCGAGGC ACAA

24

T02090-04094-0000

## (2) INFORMATION FOR SEQ. ID NO: 43

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Tm 13.17 lower primer with XhoI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAGTGGTCAA CTAAC TGAGC TCGCC 25

09076348.060704



- (2) INFORMATION FOR SEQ. ID NO: 45
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Consensus of Seq ID #44 with Tm 13.17
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
|------------|------------|--------|-----|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|
| GGCANRNNNN | AAR        | ATG    | AAR | YTN        | CTC        | TNN        | TGY        | YTN | RYN | TYC | NYC | RYY | 46  |     |     |
|            | Met        | Lys    | Leu | Leu        | Leu        | Cys        | Phe        | Ala | Phe | Ala | Ala |     |     |     |     |
|            |            |        |     |            | -15        |            |            |     |     | -10 |     |     |     |     |     |
| NTN        | NTN        | RTC    | RNA | GYT        | CAG        | GCT        | ACC        | GAN | GNA | CAR | ATN | NAG | AAA | 91  |     |
| Ile        | Val        | Ile    | Gly | Ala        | Gln        | Ala        | Leu        | Thr | Asp | Glu | Gln | Ile | Gln | Lys |     |
|            |            | -5     |     |            |            | 1          |            |     |     | 5   |     |     |     |     |     |
| NNG        | AAC        | AAG    | ATC | AGC        | AAA        | RAR        | TGY        | CAR | NAN | GNR | NNY | GGA | GTG | TCN | 136 |
| Arg        | Asn        | Lys    | Ile | Ser        | Lys        | Glu        | Cys        | Gln | Gln | Val | Ser | Gly | Val | Ser |     |
|            | 10         |        |     |            |            | 15         |            |     |     |     | 20  |     |     |     |     |
| CAA        | GAG        | AYN    | ATN | RNC        | AAA        | GYT        | CGC        | ANN | GGT | GNC | TNG | GNN | GAY | GAT | 181 |
| Gln        | Glu        | Thr    | Ile | Asp        | Lys        | Val        | Arg        | Thr | Gly | Val | Leu | Val | Asp | Asp |     |
|            | 25         |        |     |            |            | 30         |            |     |     |     | 35  |     |     |     |     |
| CCY        | AAA        | NTG    | AAR | NRN        | CAN        | GTY        | YTY        | TGC | NTN | NCN | ARG | ARN | RCY | GGN | 226 |
| Pro        | Lys        | Met    | Lys | Lys        | His        | Val        | Leu        | Cys | Phe | Ser | Lys | Lys | Thr | Gly |     |
|            | 40         |        |     |            |            | 45         |            |     |     |     | 50  |     |     |     |     |
| NTG        | GCN        | ACN    | GAA | NCN        | GGA        | GAN        | RYN        | RNN | GTN | GAN | GTR | YTN | ARR | GNN | 271 |
| Val        | Ala        | Thr    | Glu | Ala        | Gly        | Asp        | Thr        | Asn | Val | Glu | Val | Leu | Lys | Ala |     |
|            | 55         |        |     |            |            | 60         |            |     |     |     | 65  |     |     |     |     |
| AAG        | NTG        | ARG    | NAN | GTN        | RCY        | RRC        | AAC        | GAC | GAA | GAR | RYN | GAN | AAR | ATC | 316 |
| Lys        | Leu        | Lys    | His | Val        | Ala        | Ser        | Asn        | Asp | Glu | Glu | Val | Asp | Lys | Ile |     |
|            | 70         |        |     |            |            | 75         |            |     |     |     | 80  |     |     |     |     |
| RTN        | NAN        | AAG    | TGC | GYN        | GTC        | AAG        | ARR        | GNV | ACN | NYN | GAR | GAR | ACG | GYN | 361 |
| Val        | Gln        | Lys    | Cys | Val        | Val        | Lys        | Lys        | Ala | Thr | Pro | Glu | Glu | Thr | Ala |     |
|            | 85         |        |     |            |            | 90         |            |     |     |     | 95  |     |     |     |     |
| TNY        | RAY        | ACY    | TTC | AAR        | NNT        | RTY        | NNN        | RAN | ARY | AAR | CCN | RAN | TTC | TCN | 406 |
| Tyr        | Asp        | Thr    | Phe | Lys        | Cys        | Ile        | Tyr        | Asp | Ser | Lys | Pro | Asp | Phe | Ser |     |
|            | 100        |        |     |            |            | 105        |            |     |     |     | 110 |     |     |     |     |
| CCN        | RTT        | GAT    | TRA | NYNNYYNNNA | YTNGNNNRNR | NTTYRANAAT | AAAGNNNNTN |     |     |     |     |     |     |     | 458 |
| Pro        | Ile        | Asp    | *   |            |            |            |            |     |     |     |     |     |     |     |     |
|            | 115        |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| TNRTNNNRNA | AAAAAAAAAA | AAAAAA |     |            |            |            |            |     |     |     |     |     |     |     | 484 |

09076340-060701

- (2) INFORMATION FOR SEQ. ID NO: 46
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v)
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Consensus of Seq ID #45 with B1/B2
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
|------------|------------|--------|-----|------------|-------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|
| GGCANRNNNN | AAR        | ATG    | AAR | YTN        | CTC         | TNN        | TGY        | YTN | RYN | TTY | NYC | RYY | 46  |     |     |
|            | Met        | Lys    | Leu | Leu        | Leu         | Cys        | Phe        | Ala | Phe | Ala | Ala |     |     |     |     |
|            |            |        |     | -15        |             |            |            |     |     |     |     | -10 |     |     |     |
| NTN        | NTN        | RTC    | NNA | GYT        | CAG         | GCT        | NTN        | ACY | NAN | GNA | NAN | NTN | NAG | NNA | 91  |
| Ile        | Val        | Ile    | Gly | Ala        | Gln         | Ala        | Leu        | Thr | Asp | Glu | Gln | Ile | Gln | Lys |     |
|            |            | -5     |     |            |             |            | 1          |     |     |     | 5   |     |     |     |     |
| NNG        | NNC        | NAR    | AYC | AGC        | RNA         | RAR        | TGY        | NAR | NNN | GNR | NNY | GGA | GTG | TCN | 136 |
| Arg        | Asn        | Lys    | Ile | Ser        | Lys         | Glu        | Cys        | Gln | Gln | Val | Ser | Gly | Val | Ser |     |
|            | 10         |        |     |            |             | 15         |            |     |     |     | 20  |     |     |     |     |
| NAA        | GAN        | RYN    | ATN | RNN        | ARA         | GYT        | CGC        | ANN | GGT | GNC | TNG | GNN | GAY | GAY | 181 |
| Gln        | Glu        | Thr    | Ile | Asp        | Lys         | Val        | Arg        | Thr | Gly | Val | Leu | Val | Asp | Asp |     |
|            | 25         |        |     |            |             | 30         |            |     |     |     | 35  |     |     |     |     |
| CCY        | AAA        | NTG    | AAR | NNN        | CAN         | NTY        | YTY        | TGC | NTN | NYN | ARG | RNN | NYT | GRN | 226 |
| Pro        | Lys        | Met    | Lys | Lys        | His         | Val        | Leu        | Cys | Phe | Ser | Lys | Lys | Thr | Gly |     |
|            | 40         |        |     |            |             | 45         |            |     |     |     | 50  |     |     |     |     |
| NTR        | GYN        | RCN    | GAA | NCN        | GGA         | GAN        | RYN        | RNN | GYN | GAN | RYR | YTN | ARR | GNN | 271 |
| Val        | Ala        | Thr    | Glu | Ala        | Gly         | Asp        | Thr        | Asn | Val | Glu | Val | Leu | Lys | Ala |     |
|            | 55         |        |     |            |             | 60         |            |     |     |     | 65  |     |     |     |     |
| AAG        | NTG        | ANG    | NRN | NNN        | NNN         | RNN        | ANN        | RNN | RAR | RAR | RYN | RRN | ARR | NTN | 316 |
| Lys        | Leu        | Lys    | His | Val        | Ala         | Ser        | Asn        | Asp | Glu | Glu | Val | Asp | Lys | Ile |     |
|            | 70         |        |     |            |             | 75         |            |     |     |     | 80  |     |     |     |     |
| NYN        | NRN        | ARN    | NNN | NNN        | NNN         | NNG        | ARN        | RNN | NYN | NNN | RAR | RNR | NNN | NNN | 361 |
| Val        | Gln        | Lys    | Cys | Val        | Val         | Lys        | Lys        | Ala | Thr | Pro | Glu | Glu | Thr | Ala |     |
|            | 85         |        |     |            |             | 90         |            |     |     |     | 95  |     |     |     |     |
| TNN        | RAN        | NYN    | YYN | AAN        | NNN         | NNY        | NNN        | RRN | ANN | ARN | CCN | RNN | TTY | TYN | 406 |
| Tyr        | Asp        | Thr    | Phe | Lys        | Cys         | Ile        | Tyr        | Asp | Ser | Lys | Pro | Asp | Phe | Ser |     |
|            | 100        |        |     |            |             | 105        |            |     |     |     | 110 |     |     |     |     |
| CNN        | RYT        | RNT    | TRN | NYNNNNNNNN | YNNNGNNNRNR | NTTYRANAAT | AAAGNNNYTN |     |     |     |     |     |     |     | 458 |
| Pro        | Ile        | Asp    | *   |            |             |            |            |     |     |     |     |     |     |     |     |
|            | 115        |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| TNRTNNNRNA | AAAAAAAAAA | AAAAAA |     |            |             |            |            |     |     |     |     |     |     |     | 484 |

- (2) INFORMATION FOR SEQ. ID NO: 47
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Consensus of Seq. ID #46 with AFP-3
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
|------------|------------|--------|-----|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|
| GGC        | NNR        | NNNN   | AAR | ATG        | AAR        | YTN        | CTC        | YNN | TGY | YTN | RYN | YYY | NYN | RYY | 46  |
|            |            |        | Met | Lys        | Leu        | Leu        | Leu        | Cys | Phe | Ala | Phe | Ala | Ala |     |     |
|            |            |        |     |            | -15        |            |            |     |     |     |     |     |     |     | -10 |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NTN        | NTN        | RYC    | NNR | RYN        | YAN        | GCT        | NTN        | ACN | NAN | RNA | NNN | NNN | NAG | NNR | 91  |
| Ile        | Val        | Ile    | Gly | Ala        | Gln        | Ala        | Leu        | Thr | Asp | Glu | Gln | Ile | Gln | Lys |     |
|            |            | -5     |     |            |            |            | 1          |     |     |     | 5   |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NNG        | NNY        | NAR    | NNC | AGC        | RNN        | RNN        | TGY        | NAR | NNN | GNN | NNY | GGA | GTR | TCN | 136 |
| Arg        | Asn        | Lys    | Ile | Ser        | Lys        | Glu        | Cys        | Gln | Gln | Glu | Ser | Gly | Val | Ser |     |
|            | 10         |        |     |            |            | 15         |            |     |     |     | 20  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NAA        | GAN        | NYN    | NTN | RNN        | ARR        | GYY        | CGC        | ANN | NGT | GNN | NNR | GNN | GAY | GAY | 181 |
| Gln        | Glu        | Thr    | Ile | Asp        | Lys        | Val        | Arg        | Thr | Gly | Val | Leu | Val | Asp | Asp |     |
|            | 25         |        |     |            |            | 30         |            |     |     |     | 35  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| CCY        | AAA        | NTG    | AAR | NNN        | CAN        | NYN        | YTY        | TGC | NTN | NYN | ARG | RNN | NYN | GRN | 226 |
| Pro        | Lys        | Met    | Lys | Lys        | His        | Val        | Leu        | Cys | Phe | Ser | Lys | Lys | Thr | Gly |     |
|            | 40         |        |     |            | 45         |            |            |     |     |     | 50  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NTN        | RYN        | RNN    | GNN | NNN        | GGN        | GAN        | NYN        | NNN | NYN | GAN | NNN | NTN | ARR | RNN | 271 |
| Val        | Ala        | Thr    | Glu | Ala        | Gly        | Asp        | Thr        | Asn | Val | Glu | Val | Leu | Lys | Ala |     |
|            | 55         |        |     |            | 60         |            |            |     |     |     | 65  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| AAR        | NTN        | ANG    | NRN | NNN        | NNN        | RNN        | RNN        | NNN | RAR | RAR | RYN | RRN | RRN | NTN | 316 |
| Lys        | Leu        | Lys    | His | Val        | Ala        | Ser        | Asn        | Asp | Glu | Glu | Val | Asp | Lys | Ile |     |
|            | 70         |        |     |            | 75         |            |            |     |     |     | 80  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NYN        | NNN        | ARN    | NNN | NNN        | NNN        | NNG        | ARN        | RNN | NYN | NNN | NAR | NNN | NNN | NNN | 361 |
| Val        | Gln        | Lys    | Cys | Val        | Val        | Lys        | Lys        | Ala | Thr | Pro | Glu | Glu | Thr | Ala |     |
|            | 85         |        |     |            | 90         |            |            |     |     |     | 95  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NNN        | RAN        | NYN    | YYN | AAN        | NNN        | NNY        | NNN        | RRN | ANN | ARN | YCN | NNN | TNN | NNN | 406 |
| Tyr        | Asp        | Thr    | Phe | Lys        | Cys        | Ile        | Tyr        | Asp | Ser | Lys | Pro | Asp | Phe | Ser |     |
|            | 100        |        |     |            |            | 105        |            |     |     |     | 110 |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| CNN        | NYN        | RNN    | TRN | NNNNNNNNNN | YNNRNNNNNN | NNNNNNNAAT | AAANNNNNNN |     |     |     |     |     |     |     | 458 |
| Pro        | Ile        | Asp    | *   |            |            |            |            |     |     |     |     |     |     |     |     |
|            | 115        |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NNNNNNNNNA | AAAAAAAAAA | AAAAAA |     |            |            |            |            |     |     |     |     |     |     |     | 484 |

## (2) INFORMATION FOR SEQ. ID NO: 48

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE:

## (ix) FEATURES

- (D) OTHER INFORMATION: Genral Consensus of Clones,  
B1, B2 and AFP-3

09876348-060701

|                   |                   |                          |                          |                          |                   |                          |                                 |                   |                          |                   |                          |                                 |                          |                          |                          |
|-------------------|-------------------|--------------------------|--------------------------|--------------------------|-------------------|--------------------------|---------------------------------|-------------------|--------------------------|-------------------|--------------------------|---------------------------------|--------------------------|--------------------------|--------------------------|
| Met               | Lys               | Leu                      | Leu                      | Leu<br>Cys               | Cys               | Phe<br>Leu               | Ala<br>Ile<br>Thr<br>Val        | Phe<br>Ser<br>Leu | Ala<br>Leu<br>Val        | Ala<br>Ile        | Ile<br>Leu               | Val<br>Leu                      | Ile<br>Val<br>Ala        | Gly<br>Thr<br>Ala        | Ala<br>Val<br>Thr        |
| -15               |                   |                          |                          |                          |                   | -10                      |                                 |                   |                          | -5                |                          |                                 |                          |                          |                          |
| Gln<br>Tyr        | Ala               | Leu<br>Ile               | Thr                      | Asp<br>Glu               | Glu<br>Ala<br>Thr | Gln<br>Asp<br>Pro        | Ile<br>Leu<br>Arg<br>5          | Gln<br>Glu        | Lys<br>Leu               | Arg<br>Leu        | Asn<br>Arg<br>Lys        | Lys<br>Gln                      | Ile<br>Thr<br>His        | Ser                      | Lys<br>Ala<br>Asp        |
| 1                 |                   |                          |                          |                          |                   |                          |                                 |                   |                          | 10                |                          |                                 |                          |                          |                          |
| Glu<br>Lys<br>Ala | Cys               | Gln<br>Lys               | Gln<br>Asn<br>Thr<br>Ala | Glu<br>Val               | Ser               | Gly                      | Val<br>Ala                      | Ser               | Gln<br>Glu               | Glu<br>Asp<br>Ala | Thr<br>Ile<br>Val<br>Ser | Ile<br>Leu                      | Asp<br>Thr<br>Lys<br>Asn | Lys<br>Arg               | Val<br>Ala               |
| 15                |                   |                          |                          | 20                       |                   |                          |                                 |                   |                          | 25                |                          |                                 |                          | 30                       |                          |
| Arg               | Thr<br>Asn<br>Lys | Gly<br>Arg               | Val<br>Asp<br>Glu        | Leu<br>Trp<br>Glu        | Val<br>Glu        | Asp                      | Asp                             | Pro               | Lys                      | Met<br>Leu        | Lys                      | Lys<br>Arg<br>Met<br>Glu        | His<br>Gln               | Val<br>Leu<br>Ala        | Leu<br>Phe               |
| 35                |                   |                          |                          |                          |                   | 40                       |                                 |                   |                          | 45                |                          |                                 |                          |                          |                          |
| Cys               | Phe<br>Val<br>Ile | Ser<br>Ala<br>Phe<br>Leu | Lys<br>Arg               | Lys<br>Arg<br>Ala<br>Asn | Thr<br>Ala<br>Leu | Gly<br>Ile<br>Glu        | Val<br>Leu<br>Ile<br>Glu<br>Phe | Ala<br>Val<br>Ile | Thr<br>Ala<br>Asp        | Glu<br>Ala        | Ala<br>Ser               | Gly                             | Asp<br>Glu               | Thr<br>Ile<br>Val<br>Phe | Asn<br>Glu<br>Val<br>Gln |
| 50                |                   |                          |                          |                          |                   | 55                       |                                 |                   |                          | 60                |                          |                                 |                          |                          |                          |
| Val<br>Ala<br>Leu | Glu<br>Asp        | Val<br>Thr<br>His        | Leu<br>Phe<br>Ile        | Lys<br>Arg               | Ala<br>Glu<br>Thr | Lys                      | Leu<br>Val<br>Phe               | Lys<br>Thr<br>Arg | His<br>Arg<br>Lys<br>Glu | Val<br>Asn        | Ala<br>Thr<br>Ser        | Ser<br>Asn<br>Asp<br>Glu<br>His | AAA<br>Asp<br>Asn<br>His | Asp<br>Pro               | Glu                      |
| 65                |                   |                          |                          |                          |                   |                          | 70                              |                   |                          |                   | 75                       |                                 |                          |                          |                          |
| Glu<br>Lys        | Val<br>Ser<br>Thr | Asp<br>Glu               | Lys<br>Asp               | Ile<br>Leu               | Val<br>Ile        | Gln<br>Glu<br>Asn<br>Ala | Lys                             | Cys               | Val<br>Ala<br>Thr        | Val               | Val                      | Lys<br>Thr                      | Lys<br>Glu<br>Arg        | Ala<br>Asp               | Thr<br>Val               |
| 80                |                   |                          |                          |                          |                   | 85                       |                                 |                   |                          | 90                |                          |                                 |                          |                          |                          |
| Glu<br>Gln        | Glu<br>Asp<br>His | Thr<br>Ser               | Ala<br>Val<br>Ser        | Tyr<br>Phe<br>Ala        | Asp<br>Glu<br>Asn | Thr<br>Val<br>Phe        | Phe<br>Thr                      | Lys               | Cys<br>Val               | Ile<br>Val        | Tyr<br>Leu<br>Met<br>His | Asp<br>Lys                      | Ser<br>Asn<br>Asp        | Lys<br>Arg               | Pro<br>Ser               |
| 95                |                   |                          |                          | 100                      |                   |                          |                                 |                   |                          | 105               |                          | 110                             |                          |                          |                          |
| Asp<br>Asn<br>Lys | Phe               | Ser<br>Phe               | Pro<br>Gly               | Ile<br>Asp<br>Val        | Asp<br>Leu        | AAA<br>Phe               | AAA<br>Val                      | *                 | *                        | *                 |                          |                                 |                          |                          |                          |
| 115               |                   |                          |                          |                          |                   |                          |                                 |                   |                          |                   |                          |                                 |                          |                          |                          |